

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 5, 2005, 09:16:41 ; Search time 1002.05 Seconds
(without alignments)
967.120 Million cell updates/sec

Title: US-09-943-115A-9

Perfect score: 20

Sequence: 1 catgccctgtctctcttta 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.ste.*

12: gb.sv.*

13: gb.un.*

14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	AX421261 Sequence
2	20	100.0	1001	6	CQ853861 Sequence
3	20	100.0	1013	9	AF181105 Homo sapi
4	20	100.0	1345	6	AR142139 Sequence
5	20	100.0	1345	6	AR142140 Sequence
6	20	100.0	1345	6	BD222974 CYP3A4 NF
7	20	100.0	1345	6	BD222975 CYP3A4 NF
8	20	100.0	1345	6	CQ776018 Sequence
9	20	100.0	1345	6	CQ790615 Sequence
10	20	100.0	1345	6	AR222893 Sequence
11	20	100.0	1345	6	AX421253 Sequence
12	20	100.0	1345	9	HUMCY23A4
13	20	100.0	6101	6	CQ806643 Sequence
14	20	100.0	11374	9	AF185589 Homo sapi
15	20	100.0	96960	6	AX706964 Sequence
16	20	100.0	96960	6	AX707894 Sequence
17	20	100.0	123778	9	ACQ69294 Homo sapi
18	20	100.0	174832	9	AF280107 Homo sapi
19	19	95.0	176766	2	AC121258 Mus muscu

20	18.4	92.0	141296	9	AL354714 Human sapi
21	18.4	92.0	150348	2	AC127477 Felis cat
22	18.4	92.0	158146	9	AC005076 Homo sapi
23	18.4	92.0	168338	2	AC143421 Macaca mu
24	18.4	92.0	170470	9	AC146392 Pan trogl
25	18.4	92.0	185053	2	AC146392 Mus muscu
26	18	90.0	4300	5	FRU243429 Fugu rubr
27	18	90.0	13293	5	FRU243430 Fugu rubr
28	18	90.0	164331	2	AC118869 Rattus no
29	18	90.0	232188	10	AL672055 Mouse DNA
30	18	90.0	233316	2	AC145168 Mus muscu
31	18	90.0	253507	2	AC096421 Rattus no
32	18	90.0	263603	2	AC111291 Rattus no
33	18	90.0	263603	2	AC111291 Rattus no
34	17.4	87.0	269409	2	AC130995 Rattus no
35	17.4	87.0	35550	9	AC105386 Homo sapi
36	17.4	87.0	68868	2	AC101770 Mus muscu
37	17.4	87.0	82309	9	AC138136 Homo sapi
38	17.4	87.0	85166	2	AC008617 Homo sapi
39	17.4	87.0	100000	9	AP000074 Homo sapi
40	17.4	87.0	109770	2	AC073763 3 Continuation (5 of
41	17.4	87.0	110000	1	AP006841-04 Continuation (3 of
42	17.4	87.0	110000	2	AC109085-0 Continuation (3 of
43	17.4	87.0	110720	2	AC138189 Mus muscu
44	17.4	87.0	110804	9	AC004748 Homo sapi
45	17.4	87.0	127361	9	AC007283 Homo sapi
46	17.4	87.0	143669	9	AP006307 Homo sapi
47	17.4	87.0	149436	2	AC118970 Rattus no
48	17.4	87.0	153384	2	AC092518 Felis cat
49	17.4	87.0	158822	2	AC136174 Rattus no
50	17.4	87.0	161498	9	AC113376 Homo sapi
51	17.4	87.0	166452	9	AC090453 Homo sapi
52	17.4	87.0	168063	8	CNS07YQ8 Oryza sat
53	17.4	87.0	168136	10	AC117803 Mus muscu
54	17.4	87.0	170607	10	AC133650 Mus muscu
55	17.4	87.0	175440	10	AC125374 Mus muscu
56	17.4	87.0	176032	2	BX510656 Danio rer
57	17.4	87.0	176542	2	AC025036 Mus muscu
58	17.4	87.0	176598	2	AC146834 Canis fam
59	17.4	87.0	182281	2	AC150213 Otolenur
60	17.4	87.0	187359	10	AC087183 Mus muscu
61	17.4	87.0	190646	2	BX649483 Mus muscu
62	17.4	87.0	191104	10	AC123860 Mus muscu
63	17.4	87.0	191191	10	AL663083 Mouse DNA
64	17.4	87.0	195954	10	AC102154 Mus muscu
65	17.4	87.0	196550	2	AC118178 Rattus no
66	17.4	87.0	198057	2	AC073719 Mus muscu
67	17.4	87.0	204324	2	AC150724 Callithr
68	17.4	87.0	212007	10	AL935060 Mouse DNA
69	17.4	87.0	222439	10	AC124505 Mus muscu
70	17.4	87.0	226601	10	AC122863 Mus muscu
71	17.4	87.0	231443	2	AC073691 Mus muscu
72	17.4	87.0	235418	2	AC126665 Rattus no
73	17.4	87.0	242810	2	AC129394 Rattus no
74	17.4	87.0	245342	2	AC130961 Rattus no
75	17.4	87.0	245539	2	AC121656 Rattus no
76	17.4	87.0	257954	10	AC122547 Mus muscu
77	17.4	87.0	286014	2	AC112125 Rattus no
78	17	85.0	24775	3	CEC27H6 Caeenorhabdi
79	17	85.0	25172	9	AF284446 Homo sapi
80	17	85.0	66715	2	AC102943 Homo sapi
81	17	85.0	94056	9	AL133192 Human DNA
82	17	85.0	110000	2	AC106983 Rattus no
83	17	85.0	133608	2	AC117753 Mus muscu
84	17	85.0	139222	2	AC135090 Rattus no
85	17	85.0	148601	2	AC149650 Bos tauru
86	17	85.0	159243	2	AC135660 Rattus no
87	17	85.0	167697	9	AC015660 Homo sapi
88	17	85.0	174265	2	AL772355 Homo sapi
89	17	85.0	178254	9	AL7731541 Human DNA
90	17	85.0	185872	9	AC091144 Homo sapi
91	17	85.0	189649	2	AC139641 Rattus no
92	17	85.0	191082	2	AC141066 Homo sapi

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OM nucleic - nucleic search, using sw model

Run on: July 5, 2005, 09:16:41 ; Search time 2642.05 Seconds
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288.142 Million cell updates/sec

Title: US-09-943-115a-9
Perfect score: 20
Sequence: 1 catgccctgtctctcttta 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hic:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gssi:*
- 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19.4	95.0	575	AZ718060	AZ718060 RPCI-24-8
C 2	18.4	92.0	544	CB089186	CB089186 qso6a07.b
C 3	18.0	90.0	691	CB525676	CB525676 UI-N-FY0-
C 4	18.0	90.0	769	CC320522	CC320522 TAM32-27E
C 5	17.4	87.0	361	AW050373	AW050373 UI-M-BHL-
C 6	17.4	87.0	382	CV514313	CV514313 TgRSTzyr0
C 7	17.4	87.0	387	BY649264	BY649264 BY649264
C 8	17.4	87.0	402	AOQ35986	AOQ35986 CIT-HSP-2
C 9	17.4	87.0	420	BE591420	BE591420 WHE1659-1
C 10	17.4	87.0	424	BB689585	BB689585 BB689585
C 11	17.4	87.0	446	BF457758	BF457758 UI-M-B21-
C 12	17.4	87.0	489	AY127534	AY127534 AY127534
C 13	17.4	87.0	501	CD544848	CD544848 B0261D03-
C 14	17.4	87.0	534	AJ685383	AJ685383 AJ685383
C 15	17.4	87.0	536	BI114963	BI114963 602862776
C 16	17.4	87.0	542	AJ774072	AJ774072 AJ774072
C 17	17.4	87.0	547	AW536535	AW536535 G010F06-
C 18	17.4	87.0	595	CB523135	CB523135 UI-N-GK0-
C 19	17.4	87.0	600	BI985487	BI985487 3142-35 M
C 20	17.4	87.0	632	BP305637	BP305637 BP305637
C 21	17.4	87.0	650	AG167439	AG167439 Pan trogl
C 22	17.4	87.0	679	BB667251	BB667251 BB667251
C 23	17.4	87.0	724	CB814986	CB814986 AGENCOURT
C 24	17.4	87.0	770	BQ804532	BQ804532 WHE3555_G

C 25	17.4	87.0	783	9	BX999657	BX999657
C 26	17.4	87.0	879	9	CL305570	CL305570
C 27	17.4	87.0	904	9	AG538427	AG538427
C 28	17.4	87.0	948	7	CN505617	CN505617
C 29	17.4	87.0	1066	8	CC283327	CC283327
C 30	17.4	87.0	1157	8	CC250523	CC250523
C 31	17.4	87.0	1168	8	CC285993	CC285993
C 32	17.4	87.0	371	8	BH302715	BH302715
C 33	17.4	87.0	459	1	AI190664	AI190664
C 34	17.4	87.0	476	8	BZ692740	BZ692740
C 35	17.4	87.0	542	8	AQ974551	AQ974551 RPCI-23-3
C 36	17.4	87.0	581	5	BP321928	BP321928 BP321928
C 37	17.4	87.0	647	8	BH026130	BH026130 RPCI-24-3
C 38	17.4	87.0	690	8	BH386665	BH386665 AG-ND-103
C 39	17.4	87.0	768	8	AZ189167	AZ189167 SP-1013-B
C 40	17.4	87.0	910	2	BE543546	BE543546 AGENCOURT
C 41	17.4	87.0	916	5	BQ735524	BQ735524 AGENCOURT
C 42	17.4	87.0	1020	8	CC221604	CC221604 CH261-3P2
C 43	17.4	87.0	272	2	BH384218	BH384218 BH384218
C 44	17.4	87.0	352	6	CD923261	CD923261 G750-107H
C 45	17.4	87.0	367	5	BY078014	BY078014 BY078014
C 46	17.4	87.0	379	9	CL401130	CL401130 ZMMBB040
C 47	17.4	87.0	379	8	AQ093947	AQ093947 HS 2199 A
C 48	17.4	87.0	388	4	BJ283135	BJ283135 BJ283135
C 49	17.4	87.0	401	1	AA881144	AA881144 VZ06H08.r
C 50	17.4	87.0	405	9	CE335380	CE335380 t19f-g88-
C 51	17.4	87.0	445	8	AQ179569	AQ179569 HS 3179 A
C 52	17.4	87.0	448	1	AJ679242	AJ679242 AJ679242
C 53	17.4	87.0	448	1	AA261020	AA261020 m277e08.r
C 54	17.4	87.0	462	4	BJ278077	BJ278077 BJ278077
C 55	17.4	87.0	470	1	AA102305	AA102305 Z19A04.r
C 56	17.4	87.0	471	2	BB796564	BB796564 BB796564
C 57	17.4	87.0	477	8	AZ238179	AZ238179 RPCI-23-8
C 58	17.4	87.0	480	1	AJ693148	AJ693148 AJ693148
C 59	17.4	87.0	482	9	CL323902	CL323902 RPCI44_46
C 60	17.4	87.0	487	4	BJ283117	BJ283117 BJ283117
C 61	17.4	87.0	492	8	AQ997051	AQ997051 RPCI-23-3
C 62	17.4	87.0	497	7	CF516018	CF516018 CAP0002_1
C 63	17.4	87.0	498	8	AQ618705	AQ618705 HS 5169 A
C 64	17.4	87.0	501	6	CA702181	CA702181 wdkic.pk0
C 65	17.4	87.0	509	4	BJ278058	BJ278058 BJ278058
C 66	17.4	87.0	522	5	BX529662	BX529662 BX529662
C 67	17.4	87.0	529	7	CO123197	CO123197 GR_EB05D
C 68	17.4	87.0	541	8	BH278914	BH278914 CH230-17J
C 69	17.4	87.0	543	8	AZ089486	AZ089486 RPCI-23-3
C 70	17.4	87.0	550	7	CF983433	CF983433 mak20a07.
C 71	17.4	87.0	561	7	CO886111	CO886111 BovGen.16
C 72	17.4	87.0	578	6	CD898377	CD898377 G174_1080
C 73	17.4	87.0	580	5	BX114808	BX114808 BX114808
C 74	17.4	87.0	600	5	BU918109	BU918109 5013-47 M
C 75	17.4	87.0	634	2	BB048419	BB048419 BB048419
C 76	17.4	87.0	637	5	BQ999225	BQ999225 QG21H13.
C 77	17.4	87.0	644	8	BH334589	BH334589 CH230-586
C 78	17.4	87.0	651	7	CN604713	CN604713 USDA_FP_1
C 79	17.4	87.0	663	9	CE275558	CE275558 t19f-g88-
C 80	17.4	87.0	668	1	AL700041	AL700041 DKFZp686A
C 81	17.4	87.0	676	6	CD689711	CD689711 EST6234 h
C 82	17.4	87.0	680	8	BZ055557	BZ055557 CH240_27F
C 83	17.4	87.0	693	3	CC552009	CC552009 CH240_437
C 84	17.4	87.0	699	6	CD898376	CD898376 G174_1080
C 85	17.4	87.0	733	7	CV100178	CV100178 FAMU_USDA
C 86	17.4	87.0	735	2	BB619744	BB619744 BB619744
C 87	17.4	87.0	745	6	CD903449	CD903449 G356_110G
C 88	17.4	87.0	753	9	CC580305	CC580305 CH240_374
C 89	17.4	87.0	765	9	AG604596	AG604596 Mus_muscul
C 90	17.4	87.0	769	9	CR166627	CR166627 Forward s
C 91	17.4	87.0	772	9	CL654808	CL654808 PRI0121c
C 92	17.4	87.0	779	9	CC509150	CC509150 CH240_351
C 93	17.4	87.0	784	8	BZ265120	BZ265120 BZ265120
C 94	17.4	87.0	787	6	CB347189	CB347189 CAB2SG000
C 95	17.4	87.0	801	6	CB346615	CB346615 CAB2SG000
C 96	17.4	87.0	807	9	AG509509	AG509509 Mus_muscul
C 97	17.4	87.0	811	9	CR084805	CR084805 Forward s

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341.524 Million cell updates/sec

Title: US-09-943-115a-9

Perfect score: 20

Sequence: 1 catgccctgtctctcttcta 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : N_Geneseq_16Dec04:*

1: Geneseq19808:*

2: Geneseq19908:*

3: Geneseq20008:*

4: Geneseq20018:*

5: Geneseq20028:*

6: Geneseq20038:*

7: Geneseq20048:*

8: Geneseq20058:*

9: Geneseq20068:*

10: Geneseq20078:*

11: Geneseq20088:*

12: Geneseq20098:*

13: Geneseq20108:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	6	Abk68753 PCR prime
2	20	100.0	1001	13	Adc81033 Human phe
3	20	100.0	1345	2	Aax28296 Human CYP
4	20	100.0	1345	3	Aaz57019 Nucleic a
5	20	100.0	1345	3	Aaz57020 Nucleic a
6	20	100.0	1345	6	Abk68745 5'-flanki
7	20	100.0	1345	12	Adj84441 Human phe
8	20	100.0	6101	13	Adc89077 Human CYP
9	20	100.0	12983	8	Aad41239 Human CYP
10	20	100.0	13035	8	Aad51997 Human CYP
11	20	100.0	15185	8	Aad52000 Human CYP
12	20	100.0	39071	12	Adm97420 Prostate
13	20	100.0	96960	8	Acfc62734 Cancer ba
14	20	100.0	96960	8	Adb20849 MRPI base
15	20	100.0	96960	10	Adb87938 Human UGT
16	20	100.0	96960	10	Adb96921 Human MDR
17	20	100.0	96960	10	Adb92112 Human MDR
18	20	100.0	123785	10	Abx77171 DNA seque
19	17.4	87.0	38358	4	Aak73535 Human imm
20	17	85.0	1025	6	Abk35006 Human cdn

C	21	16.8	84.0	192	2	AAV75862	Aav75862 Staphyloc
	22	16.8	84.0	1847	5	AAS69462	Aas69462 DNA encod
	23	16.8	84.0	2119	5	AAS88184	Aas88184 DNA encod
	24	16.8	84.0	2204	2	AAT84019	Aat84019 DNA encod
C	25	16.8	84.0	6101	13	ADS89690	Ads89690 Oligonuc
C	26	16.8	84.0	6101	13	ADS89416	Ads89416 Oligonuc
C	27	16.8	84.0	34637	10	AAD64732	Aad64732 Mouse car
	28	16.8	84.0	37135	9	ADA02645	Ada02645 Mouse Tbx
	29	16.8	84.0	37135	10	ADB72383	Adb72383 Mouse Tbx
	30	16.8	84.0	37135	10	ADE95893	Ade95893 Mouse Tbx
	31	16.8	84.0	87687	11	ACN45166	Acn45166 Human gen
	32	16.8	84.0	138	5	ABV15553	Abv15553 Human pro
	33	16.4	82.0	245	5	ABV06384	Abv06384 Human pro
	34	16.4	82.0	556	5	ABV36343	Abv36343 Human pro
	35	16.4	82.0	556	5	ABV45374	Abv45374 Human pro
	36	16.4	82.0	565	5	ABV98930	Abv98930 Human pan
C	37	16.4	82.0	791	5	ABV24075	Abv24075 Human pro
C	38	16.4	82.0	791	5	ABV29956	Abv29956 Human pro
C	39	16.4	82.0	1567	6	AAS18588	Aas18588 CDNA enco
	40	16.4	82.0	2158	3	ACG93483	Acg93483 Human sec
C	41	16.4	82.0	2164	12	ADL61106	Adl61106 Human tyr
C	42	16.4	82.0	2207	4	AAH18125	Aah18125 Human cdn
C	43	16.4	82.0	2267	3	AAC59489	Aac59489 Human sec
C	44	16.4	82.0	2749	6	ABK35261	Abk35261 Human cdn
C	45	16.4	82.0	2783	2	AZ333566	Aaz333566 Human bre
C	46	16.4	82.0	2905	4	AAI58169	Aai58169 Human pol
C	47	16.4	82.0	2905	5	AQ98375	Adq98375 DNA encod
C	48	16.4	82.0	2905	5	ADB48135	Adb48135 Novel hum
C	49	16.4	82.0	3465	5	AA72746	Aa72746 DNA encod
C	50	16.4	82.0	3543	4	AAF55697	Aaf55697 Human EPL
C	51	16.4	82.0	3650	4	AAF55697	Aaf55697 Human EPL
C	52	16.4	82.0	3655	8	ACF34552	Acf34552 Gene enco
C	53	16.4	82.0	3655	13	ACN39434	Acn39434 Tumour-as
C	54	16.4	82.0	3664	5	ABX71307	Abx71307 Human tra
C	55	16.4	82.0	3705	3	AA53826	Aas53826 Sequence
C	56	16.4	82.0	3711	3	AA77143	Aac77143 Human ORF
C	57	16.4	82.0	3776	12	ADQ63943	Adq63943 Novel hum
	58	16.4	82.0	4003	4	AAK76291	Aak76291 Human imm
	59	16.4	82.0	4003	4	AAK76397	Aak76397 Human imm
	60	16.4	82.0	4044	4	AAK76292	Aak76292 Human imm
	61	16.4	82.0	4044	4	AAK76399	Aak76399 Human imm
C	62	16.4	82.0	16552	4	AAK91417	Aak91417 Human dig
C	63	16.4	82.0	16552	4	AAK91416	Aak91416 Human dig
C	64	16.4	82.0	16552	4	AAI57784	Aai57784 Human col
C	65	16.4	82.0	16552	4	AAI57785	Aai57785 Human col
C	66	16.4	82.0	16552	6	ABS99961	Abs99961 Genomic D
C	67	16.4	82.0	16552	6	ABS99962	Abs99962 Genomic D
C	68	16.4	82.0	16552	10	ADB93114	Adb93114 Human col
C	69	16.4	82.0	16552	10	ADB93115	Adb93115 Human col
C	70	16.4	82.0	60202	12	ADQ97340	Adq97340 Mouse can
C	71	16.4	82.0	110000	13	ABD32629	Abd32629 Continuation (3 of
	72	16.4	82.0	14179	11	ACN44188	Acn44188 Mouse gen
	73	16.4	82.0	319608	3	AAH51601	Aah51601 Human chr
	74	16.4	82.0	319608	5	AAS09301	Aas09301 Human sch
	75	16	80.0	363	2	AAT31760	Aat31760 Liver exp
	76	16	80.0	363	13	ADR41664	Adr41664 Human.liv
	77	16	80.0	503	2	AAV43784	Aav43784 Primate C
	78	16	80.0	570	10	ACA55449	Aca55449 Human sig
	79	16	80.0	570	12	ADI55245	Adi55245 Human pol
	80	16	80.0	103665	12	ADQ97703	Adq97703 Human can
C	81	15.8	79.0	329	4	AAK89026	Aak89026 Human dig
C	82	15.8	79.0	329	5	AAK89026	Aak89026 Genomic s
C	83	15.8	79.0	329	9	ADB32585	Adb32585 Human nov
C	84	15.8	79.0	364	10	ADF80985	Adf80985 Leukaemia
C	85	15.8	79.0	392	5	ADL62238	Adl62238 Human ova
	86	15.8	79.0	402	5	AAF64773	Aaf64773 Novel hum
C	87	15.8	79.0	443	5	ADI76110	Adi76110 Human ova
C	88	15.8	79.0	443	5	ADI69773	Adi69773 Human ova
	89	15.8	79.0	480	4	AAH84070	Aah84070 Pongo pyg
C	90	15.8	79.0	524	6	AAH39681	Aah39681 Human sec
	91	15.8	79.0	537	12	ADQ21343	Adq21343 Human sof
C	92	15.8	79.0	542	10	ADP82362	Adp82362 Leukaemia
C	93	15.8	79.0	543	5	ADL41346	Adl41346 Human ova

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OM nucleic - nucleic search, using sw model

Run on: July .5, 2005, 09:16:41 ; Search time 101.538 Seconds
(without alignments)
322.297 Million cell updates/sec

Title: US-09-943-115A-9
Perfect score: 20
Sequence: 1 catgcccgtctctccttta 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents NA.*
1: /cgm2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgm2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgm2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgm2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgm2_6/ptodata/1/ina/PTUS_COMB.seq:*
6: /cgm2_6/ptodata/1/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	1345	3	US-09-372-339-1
2	20	100.0	1345	3	US-09-372-339-2
3	20	100.0	1345	3	US-09-144-367-3
4	20	100.0	31197	4	US-09-949-016-12963
5	20	100.0	103934	4	US-09-949-016-14433
6	18.4	92.0	35064	4	US-09-949-016-12778
7	18.4	92.0	35065	4	US-09-949-016-13196
8	17	85.0	601	4	US-09-949-016-59559
9	17	85.0	29172	4	US-09-949-016-15520
10	16.8	84.0	192	4	US-08-956-171E-1551
11	16.8	84.0	192	4	US-08-781-986A-1551
12	16.8	84.0	397	4	US-09-621-976-17859
13	16.8	84.0	72278	4	US-09-949-016-16113
14	16.8	84.0	421118	4	US-09-949-016-16297
15	16.4	82.0	601	4	US-09-949-016-107834
16	16.4	82.0	2905	4	US-09-620-312D-45
17	16.4	82.0	319608	4	US-09-539-333D-1
18	16.4	82.0	319608	4	US-09-679-409-1
19	16.4	82.0	390890	4	US-09-949-016-14720
20	16	80.0	363	1	US-08-347-492B-1
21	16	80.0	363	2	US-08-798-143-1
22	16	80.0	363	5	PCT-US95-15484-1
23	16	80.0	570	4	US-09-016-434-47
24	16	80.0	577	5	PCT-US95-07171-1
25	15.8	79.0	601	4	US-09-949-016-37725
26	15.8	79.0	601	4	US-09-949-016-37726
27	15.8	79.0	601	4	US-09-949-016-38228

15.8	79.0	601	4	US-09-949-016-76282	Sequence 76282, A
15.8	79.0	601	4	US-09-949-016-76283	Sequence 76283, A
15.8	79.0	601	4	US-09-949-016-78795	Sequence 78795, A
15.8	79.0	601	4	US-09-949-016-78796	Sequence 78796, A
15.8	79.0	601	4	US-09-949-016-113084	Sequence 113084, A
15.8	79.0	601	4	US-09-949-016-146833	Sequence 146833, A
15.8	79.0	601	4	US-09-949-016-159915	Sequence 159915, A
15.8	79.0	601	4	US-09-949-016-159936	Sequence 159936, A
15.8	79.0	601	4	US-09-949-016-175088	Sequence 175088, A
15.8	79.0	857	4	US-09-673-395A-49	Sequence 49, Appl
15.8	79.0	2880	1	US-08-158-189-1	Sequence 1, Appl
15.8	79.0	4937	4	US-09-949-016-4121	Sequence 4121, Ap
15.8	79.0	5348	4	US-09-949-016-17509	Sequence 17509, A
15.8	79.0	5349	4	US-09-949-016-12206	Sequence 12206, A
15.8	79.0	6674	4	US-09-620-312D-110	Sequence 110, App
15.8	79.0	7292	4	US-09-949-016-14862	Sequence 14862, A
15.8	79.0	12157	4	US-09-949-016-13490	Sequence 13490, A
15.8	79.0	12157	4	US-09-949-016-13491	Sequence 13491, A
15.8	79.0	12157	4	US-09-949-016-15709	Sequence 15709, A
15.8	79.0	12157	4	US-09-949-016-15710	Sequence 15710, A
15.8	79.0	12928	4	US-09-949-016-12772	Sequence 12772, A
15.8	79.0	12928	4	US-09-949-016-16702	Sequence 16702, A
15.8	79.0	14516	4	US-09-949-016-17047	Sequence 17047, A
15.8	79.0	16056	4	US-09-949-016-16211	Sequence 16211, A
15.8	79.0	16056	4	US-09-949-016-16212	Sequence 16212, A
15.8	79.0	29771	4	US-09-949-016-12754	Sequence 12754, A
15.8	79.0	29771	4	US-09-949-016-13956	Sequence 13956, A
15.8	79.0	36820	4	US-09-949-016-16665	Sequence 16665, A
15.8	79.0	42000	4	US-10-081-563-25	Sequence 25, Appl
15.8	79.0	44676	4	US-09-949-016-17511	Sequence 17511, A
15.8	79.0	51698	4	US-09-949-016-12671	Sequence 12671, A
15.8	79.0	57507	4	US-09-949-016-15019	Sequence 15019, A
15.8	79.0	70770	4	US-09-949-016-16938	Sequence 16938, A
15.8	79.0	96340	4	US-09-949-016-15863	Sequence 15863, A
15.8	79.0	113100	4	US-09-949-016-12245	Sequence 12245, A
15.8	79.0	134140	4	US-09-949-016-12672	Sequence 12672, A
15.8	79.0	134241	4	US-09-949-016-12674	Sequence 12674, A
15.8	79.0	134242	4	US-09-949-016-15813	Sequence 15813, A
15.8	79.0	134242	4	US-09-949-016-15814	Sequence 15814, A
15.8	79.0	134242	4	US-09-949-016-15815	Sequence 15815, A
15.8	79.0	176006	4	US-09-949-016-16804	Sequence 16804, A
15.8	79.0	200663	4	US-09-949-016-12569	Sequence 12569, A
15.8	79.0	232024	4	US-09-949-016-13477	Sequence 13477, A
15.8	79.0	253375	4	US-09-949-016-12849	Sequence 12849, A
15.8	79.0	392000	4	US-10-027-983-11	Sequence 11, Appl
15.8	79.0	784019	4	US-09-949-016-14033	Sequence 14033, A
15.8	79.0	828152	4	US-09-949-016-12777	Sequence 12777, A
15.4	77.0	370	4	US-09-640-211A-1483	Sequence 1483, Ap
15.4	77.0	478	4	US-09-640-211A-218	Sequence 218, App
15.4	77.0	601	4	US-09-949-016-59777	Sequence 59777, A
15.4	77.0	601	4	US-09-949-016-59781	Sequence 59781, A
15.4	77.0	601	4	US-09-949-016-140249	Sequence 140249, A
15.4	77.0	601	4	US-09-949-016-140253	Sequence 140253, A
15.4	77.0	601	4	US-09-949-016-159914	Sequence 159914, A
15.4	77.0	601	4	US-09-949-016-159935	Sequence 159935, A
15.4	77.0	601	4	US-09-949-016-192817	Sequence 192817, A
15.4	77.0	601	4	US-09-949-016-203973	Sequence 203973, A
15.4	77.0	988	4	US-09-774-528-432	Sequence 432, App
15.4	77.0	1162	1	US-08-474-140-14	Sequence 14, Appl
15.4	77.0	1162	1	US-08-477-630-14	Sequence 14, Appl
15.4	77.0	1162	1	US-08-472-293-14	Sequence 14, Appl
15.4	77.0	1162	1	US-08-474-545-14	Sequence 14, Appl
15.4	77.0	1162	1	US-08-478-341-14	Sequence 14, Appl
15.4	77.0	1162	3	US-08-996-733-14	Sequence 14, Appl
15.4	77.0	2370	4	US-09-873-404-1	Sequence 1, Appl
15.4	77.0	2370	4	US-10-343-735-1	Sequence 1, Appl
15.4	77.0	3167	4	US-09-949-001-7	Sequence 7, Appl
15.4	77.0	3198	4	US-09-949-001-2	Sequence 2, Appl
15.4	77.0	4060	1	US-08-308-949A-1	Sequence 1, Appl
15.4	77.0	4464	1	US-08-474-140-8	Sequence 8, Appl
15.4	77.0	4464	1	US-08-474-140-9	Sequence 9, Appl
15.4	77.0	4464	1	US-08-477-630-8	Sequence 8, Appl
15.4	77.0	4464	1	US-08-477-630-9	Sequence 9, Appl

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OM nucleic - nucleic search, using sw model

Run on: July 5, 2005, 10:04:06 ; Search time 3937.44 Seconds
(without alignments)
31.859 Million cell updates/sec

Title: US-09-943-115A-9

Perfect score: 20

Sequence: 1 catgcccgtctctcttta 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6313374 seqs, 3136092125 residues

Total number of hits satisfying chosen parameters: 12626748

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications NA.*

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6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
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9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09D_PUBCOMB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
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26: /cgn2_6/ptodata/1/pubpna/US11C_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	10	US-09-943-115A-9
2	20	100.0	1345	14	US-09-943-115A-1
3	20	100.0	1345	14	US-10-146-575-3
4	20	100.0	1345	14	US-10-085-612-3
5	20	100.0	12983	21	US-10-415-607-1
6	20	100.0	13035	15	US-10-121-960C-14
7	20	100.0	15185	15	US-10-121-960C-17

20	100.0	96960	21	US-10-484-577-662	Sequence 662, App
17	85.0	1025	9	US-09-822-849A-144	Sequence 144, App
16.8	84.0	192	8	US-08-781-986A-1551	Sequence 1551, Ap
16.8	84.0	192	18	US-10-329-624-1551	Sequence 1551, Ap
16.8	84.0	611	13	US-10-027-632-219495	Sequence 219495, Ap
16.8	84.0	611	17	US-10-027-632-219495	Sequence 219495, Ap
16.8	84.0	646	13	US-10-027-632-247126	Sequence 247126, Ap
16.8	84.0	646	17	US-10-027-632-247126	Sequence 247126, Ap
16.8	84.0	1071	13	US-10-027-632-256517	Sequence 256517, Ap
16.8	84.0	1071	17	US-10-027-632-256517	Sequence 256517, Ap
16.8	84.0	1071	17	US-10-027-632-256518	Sequence 256518, Ap
16.8	84.0	2122	18	US-10-424-599-119619	Sequence 119619, Ap
16.8	84.0	33988	19	US-10-741-601-5670	Sequence 5670, Ap
16.8	84.0	33988	21	US-10-741-601-5670	Sequence 17701, A
16.8	84.0	37135	18	US-10-052-482-151	Sequence 151, App
16.8	84.0	87687	13	US-10-087-192-1978	Sequence 1978, Ap
16.8	84.0	138	20	US-10-357-930-15544	Sequence 15544, A
16.4	82.0	177	17	US-10-242-535A-15202	Sequence 15202, A
16.4	82.0	177	18	US-10-085-783A-15202	Sequence 15202, A
16.4	82.0	228	9	US-09-783-590-176	Sequence 176, App
16.4	82.0	245	20	US-10-357-930-6375	Sequence 6375, Ap
16.4	82.0	382	17	US-10-242-535A-36128	Sequence 36128, A
16.4	82.0	382	18	US-10-085-783A-36128	Sequence 36128, A
16.4	82.0	549	13	US-10-027-632-51536	Sequence 51536, A
16.4	82.0	549	13	US-10-027-632-51537	Sequence 51537, A
16.4	82.0	549	13	US-10-027-632-53794	Sequence 53794, A
16.4	82.0	549	13	US-10-027-632-53795	Sequence 53795, A
16.4	82.0	549	13	US-10-027-632-321440	Sequence 321440, A
16.4	82.0	549	13	US-10-027-632-321441	Sequence 321441, A
16.4	82.0	549	13	US-10-027-632-321441	Sequence 321441, A
16.4	82.0	556	20	US-10-357-930-36361	Sequence 36361, A
16.4	82.0	556	20	US-10-357-930-45393	Sequence 45393, A
16.4	82.0	791	20	US-10-060-036-4338	Sequence 4338, Ap
16.4	82.0	791	20	US-10-357-930-24064	Sequence 24064, A
16.4	82.0	791	20	US-10-357-930-29974	Sequence 29974, A
16.4	82.0	820	13	US-10-027-632-154192	Sequence 154192, A
16.4	82.0	820	13	US-10-027-632-154192	Sequence 154192, A
16.4	82.0	820	17	US-10-648-593-30	Sequence 30, Appl
16.4	82.0	2164	19	US-10-037-270-45	Sequence 30, Appl
16.4	82.0	2432	13	US-10-027-632-103097	Sequence 103097, A
16.4	82.0	2432	13	US-10-027-632-111848	Sequence 111848, A
16.4	82.0	2432	17	US-10-027-632-103097	Sequence 103097, A
16.4	82.0	2432	17	US-10-027-632-111848	Sequence 111848, A
16.4	82.0	2749	9	US-09-822-849A-399	Sequence 399, App
16.4	82.0	2905	15	US-10-037-270-45	Sequence 45, Appl
16.4	82.0	2905	17	US-10-117-722-45	Sequence 45, Appl
16.4	82.0	3543	10	US-09-783-732-1	Sequence 1, Appl
16.4	82.0	3550	21	US-10-958-157-4290	Sequence 1, Appl
16.4	82.0	3650	10	US-09-783-732-3	Sequence 3, Appl
16.4	82.0	3655	21	US-10-489-740-107	Sequence 107, App
16.4	82.0	3655	21	US-10-956-157-2109	Sequence 2109, App
16.4	82.0	3655	21	US-10-956-157-2109	Sequence 321, App
16.4	82.0	16552	9	US-09-764-855-321	Sequence 321, App
16.4	82.0	16552	14	US-10-072-349-321	Sequence 321, App
16.4	82.0	16552	14	US-10-072-349-322	Sequence 322, App
16.4	82.0	144179	13	US-10-087-192-511	Sequence 511, App
16.4	82.0	319608	17	US-10-147-603-1	GENERAL INFORMATI
16.4	82.0	518360	19	US-10-367-094-125	Sequence 125, App
16	80.0	181	18	US-10-424-599-35871	Sequence 35871, A
16	80.0	363	14	US-10-293-705-1	Sequence 1, Appl
16	80.0	363	20	US-10-779-267-1	Sequence 1, Appl
16	80.0	570	17	US-10-305-720-47	Sequence 47, Appl
16	80.0	16998	21	US-10-741-600-17978	Sequence 17978, A
16	80.0	30431	21	US-10-741-600-17746	Sequence 17746, A
15	79.0	217	18	US-10-424-599-123925	Sequence 123925, A
15.8	79.0	250	9	US-09-783-590-7843	Sequence 7843, Ap
15.8	79.0	329	10	US-09-764-872-522	Sequence 522, App
15.8	79.0	392	10	US-09-814-353-20450	Sequence 20450, A

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OM nucleic - nucleic search, using sw model

Run on: July 5, 2005, 09:16:41 ; Search time 951.949 Seconds
(without alignments)
967.120 Million cell updates/sec

Title: US-09-943-115A-10

Perfect score: 19

Sequence: 1 ccattcccttcgcaatc 19

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

GenEmbl:**

1: gb_ba:**

2: gb_htg:**

3: gb_in:**

4: gb_om:**

5: gb_ov:**

6: gb_pat:**

7: gb_ph:**

8: gb_pl:**

9: gb_pr:**

10: gb_ro:**

11: gb_sts:**

12: gb_sy:**

13: gb_un:**

14: gb_vi:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	19	6	AX421262 Sequence
2	19	100.0	1013	9	AF181105 Homo sapi
3	19	100.0	1345	6	AR142139 Sequence
4	19	100.0	1345	6	AR142140 Sequence
5	19	100.0	1345	6	BD222974 CYP3A4 NF
6	19	100.0	1345	6	BD222975 CYP3A4 NF
7	19	100.0	1345	6	CQ776018 Sequence
8	19	100.0	1345	6	CQ790615 Sequence
9	19	100.0	1345	6	AR222893 Sequence
10	19	100.0	1345	6	AX421253 Sequence
11	19	100.0	1345	9	HUMCYP3A4
12	19	100.0	6101	6	CQ806643 Sequence
13	19	100.0	11374	9	AF185589 Homo sapi
14	19	100.0	96960	6	AX706964 Sequence
15	19	100.0	96960	6	AX707894 Sequence
16	19	100.0	123778	9	AC069294 Homo sapi
17	19	100.0	170470	9	AC146392 Pan trogl
18	19	100.0	174832	9	AF280107 Homo sapi
19	17.4	91.6	1652	8	AY598939 Aspergill

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OM nucleic - nucleic search, using sw model

Run on: July 5, 2005, 10:04:06 ; Search time 3740.56 Seconds
(without alignments)
31.859 Million cell updates/sec

Title: US-09-943-115A-10

Perfect score: 19

Sequence: 1 ccatcccttcgcaatc 19

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6313374 seqs, 3136092125 residues

Total number of hits satisfying chosen parameters: 12626748

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match: 0%

Maximum Match: 100%

Listing first 1000 summaries

Database : Published Applications NA.*

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2:	/cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
3:	/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4:	/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5:	/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6:	/cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
7:	/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8:	/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9:	/cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10:	/cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11:	/cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12:	/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13:	/cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14:	/cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15:	/cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16:	/cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17:	/cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18:	/cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19:	/cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
20:	/cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
21:	/cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
22:	/cgn2_6/ptodata/1/pubpna/US10J_PUBCOMB.seq.*
23:	/cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
24:	/cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
25:	/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
26:	/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	10	US-09-943-115A-10
2	19	100.0	1345	10	US-09-943-115A-10
3	19	100.0	1345	14	US-10-146-575-3
4	19	100.0	1345	14	US-10-146-575-3
5	19	100.0	12983	21	US-10-085-612-3
6	19	100.0	13035	15	US-10-415-607-1
7	19	100.0	15185	15	US-10-121-960C-14
					US-10-121-960C-17
					Sequence 10, Appli
					Sequence 1, Appli
					Sequence 3, Appli
					Sequence 1, Appli
					Sequence 14, Appli
					Sequence 17, Appli

C	8	19	100.0	96960	21	US-10-484-577-662	Sequence 662, App
C	9	16.4	86.3	309	15	US-10-106-698-4240	Sequence 4240, App
C	10	16.4	86.3	460	13	US-10-027-632-39686	Sequence 39686, A
C	11	16.4	86.3	460	17	US-10-027-632-39686	Sequence 39686, A
C	12	16.4	86.3	520	16	US-10-029-386-8303	Sequence 8303, App
C	13	16.4	86.3	568	13	US-10-027-632-39434	Sequence 39434, App
C	14	16.4	86.3	568	13	US-10-027-632-39435	Sequence 39435, A
C	15	16.4	86.3	568	17	US-10-027-632-39434	Sequence 39434, A
C	16	16.4	86.3	568	17	US-10-027-632-39435	Sequence 39435, A
C	17	16.4	86.3	1012	9	US-09-957-997-4	Sequence 4, Appli
C	18	16.4	86.3	8943	17	US-10-257-166-47	Sequence 47, Appli
C	19	16.4	86.3	11186	9	US-09-957-997-1	Sequence 1, Appli
C	20	16.4	86.3	11186	21	US-10-415-607-4	Sequence 4, Appli
C	21	16.4	86.3	258493	13	US-10-087-192-1000	Sequence 1000, App
C	22	16	84.2	810	20	US-10-425-115-67010	Sequence 67010, App
C	23	16	84.2	1036	18	US-10-425-114-28486	Sequence 28486, A
C	24	16	84.2	1090	20	US-10-425-115-67013	Sequence 67013, A
C	25	16	84.2	1146	20	US-10-425-115-67012	Sequence 67012, A
C	26	15.8	83.2	369	20	US-10-425-115-128026	Sequence 128026, A
C	27	15.8	83.2	416	19	US-10-767-701-10968	Sequence 10968, A
C	28	15.8	83.2	421	18	US-10-424-599-122852	Sequence 122852, A
C	29	15.8	83.2	446	9	US-09-954-456-436	Sequence 436, App
C	30	15.8	83.2	446	9	US-09-954-456-2188	Sequence 2188, App
C	31	15.8	83.2	446	9	US-09-967-768A-273	Sequence 273, App
C	32	15.8	83.2	446	21	US-10-843-641A-3463	Sequence 3463, App
C	33	15.8	83.2	446	21	US-10-843-641A-5215	Sequence 5215, App
C	34	15.8	83.2	446	21	US-10-843-641A-6418	Sequence 6418, App
C	35	15.8	83.2	489	19	US-10-437-963-61363	Sequence 61363, A
C	36	15.8	83.2	490	20	US-10-425-115-109271	Sequence 109271, A
C	37	15.8	83.2	501	9	US-09-833-790-172	Sequence 172, App
C	38	15.8	83.2	520	13	US-10-027-632-193809	Sequence 193809, A
C	39	15.8	83.2	520	13	US-10-027-632-193810	Sequence 193810, A
C	40	15.8	83.2	520	13	US-10-027-632-193811	Sequence 193811, A
C	41	15.8	83.2	520	17	US-10-027-632-193809	Sequence 193809, A
C	42	15.8	83.2	520	17	US-10-027-632-193810	Sequence 193810, A
C	43	15.8	83.2	520	17	US-10-027-632-193811	Sequence 193811, A
C	44	15.8	83.2	671	20	US-10-425-115-104327	Sequence 104327, A
C	45	15.8	83.2	747	13	US-10-027-632-151802	Sequence 151802, A
C	46	15.8	83.2	747	17	US-10-027-632-151802	Sequence 151802, A
C	47	15.8	83.2	752	20	US-10-357-930-12875	Sequence 12875, A
C	48	15.8	83.2	835	13	US-10-027-632-136499	Sequence 136499, A
C	49	15.8	83.2	835	13	US-10-027-632-136500	Sequence 136500, A
C	50	15.8	83.2	835	17	US-10-027-632-136499	Sequence 136499, A
C	51	15.8	83.2	835	17	US-10-027-632-136500	Sequence 136500, A
C	52	15.8	83.2	1119	20	US-10-767-701-13354	Sequence 13354, A
C	53	15.8	83.2	1193	20	US-10-425-115-41894	Sequence 41894, A
C	54	15.8	83.2	1395	19	US-10-767-701-10967	Sequence 10967, A
C	55	15.8	83.2	1990	17	US-10-094-749-15	Sequence 15, Appl
C	56	15.8	83.2	2214	17	US-10-094-749-15	Sequence 15, Appl
C	57	15.8	83.2	4205	19	US-10-437-963-74913	Sequence 74913, A
C	58	15.8	83.2	5840	9	US-09-070-927A-31	Sequence 31, Appl
C	59	15.8	83.2	185555	13	US-10-087-192-1999	Sequence 1999, App
C	60	15.4	81.1	680	19	US-10-437-963-18185	Sequence 18185, A
C	61	15.4	81.1	785	18	US-10-425-114-17866	Sequence 17866, A
C	62	15.4	81.1	789	18	US-10-425-114-17877	Sequence 17877, A
C	63	15.4	81.1	870	13	US-10-027-632-122215	Sequence 122215, A
C	64	15.4	81.1	870	17	US-10-027-632-122215	Sequence 122215, A
C	65	15.4	81.1	1000	13	US-10-027-632-118796	Sequence 118796, A
C	66	15.4	81.1	1000	17	US-10-027-632-118796	Sequence 118796, A
C	67	15.4	81.1	1002	13	US-10-027-632-121793	Sequence 121793, A
C	68	15.4	81.1	1002	13	US-10-027-632-121794	Sequence 121794, A
C	69	15.4	81.1	1002	13	US-10-027-632-121795	Sequence 121795, A
C	70	15.4	81.1	1002	17	US-10-027-632-121793	Sequence 121793, A
C	71	15.4	81.1	1002	17	US-10-027-632-121794	Sequence 121794, A
C	72	15.4	81.1	1002	17	US-10-027-632-121795	Sequence 121795, A
C	73	15.4	81.1	1102	18	US-10-424-599-23518	Sequence 23518, A
C	74	15.4	81.1	1974	18	US-10-425-114-7998	Sequence 7998, App
C	75	15.4	81.1	2024	20	US-10-425-115-29365	Sequence 29365, A
C	76	15.4	81.1	2139	17	US-10-282-122A-30885	Sequence 30885, A
C	77	15.4	81.1	2380	17	US-10-454-199-25	Sequence 25, Appl
C	78	15.4	81.1	2940	19	US-10-437-963-22374	Sequence 22374, A
C	79	15.4	81.1	4059	18	US-10-424-599-23519	Sequence 23519, A
C	80	15.4	81.1	45839	13	US-10-025-187-3	Sequence 3, Appli

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OM nucleic - nucleic search, using sw model

Run on: July 5, 2005, 09:16:41 ; Search time 96.4615 Seconds
(without alignments)
322.297 Million cell updates/sec

Title: US-09-943-115A-10
Perfect score: 19
Sequence: 1 ccattcccttcgaatc 19

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents NA.*
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5: /cgn2_6/ptodata/1/ina/PTCUS-COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	19	100.0	1345	3	US-09-372-339-1
C 2	19	100.0	1345	3	US-09-372-339-2
C 3	19	100.0	1345	3	US-09-144-367-3
C 4	19	100.0	31197	4	US-09-949-016-12963
C 5	19	100.0	103934	4	US-09-949-016-14433
C 6	16.4	85.3	34172	4	US-09-949-016-14432
C 7	15.8	83.2	389	4	US-09-513-999C-21877
C 8	15.8	83.2	594	4	US-09-134-000C-2075
C 9	15.8	83.2	663	4	US-09-902-540-1693
C 10	15.8	83.2	73757	4	US-09-949-016-15369
C 11	15.4	81.1	601	4	US-09-949-016-89049
C 12	15.4	81.1	2380	4	US-09-436-699C-25
C 13	15.4	81.1	9649	4	US-09-949-016-15672
C 14	15.4	81.1	27317	4	US-09-949-016-11955
C 15	15.4	81.1	49399	4	US-09-949-016-13780
C 16	15.4	81.1	162465	4	US-09-949-016-14264
C 17	15	78.9	882	4	US-09-489-039A-2691
C 18	15	78.9	1389	4	US-09-351-150A-22
C 19	15	78.9	8841	4	US-09-949-016-14996
C 20	15	78.9	11668	4	US-09-949-016-11878
C 21	15	78.9	11713	4	US-09-949-016-13554
C 22	15	78.9	24494	4	US-09-351-150A-1
C 23	14.8	77.9	246	4	US-09-248-796A-10333
C 24	14.8	77.9	546	4	US-09-902-540-5427
C 25	14.8	77.9	548	4	US-09-573-080A-268
C 26	14.8	77.9	601	4	US-09-949-016-48798
C 27	14.8	77.9	601	4	US-09-949-016-48970

C 28	14.8	77.9	601	4	US-09-949-016-49142	Sequence 49142, A
C 29	14.8	77.9	601	4	US-09-949-016-49318	Sequence 49318, A
C 30	14.8	77.9	601	4	US-09-949-016-89071	Sequence 89071, A
C 31	14.8	77.9	601	4	US-09-949-016-167922	Sequence 167922, A
C 32	14.8	77.9	601	4	US-09-949-016-167923	Sequence 167923, A
C 33	14.8	77.9	601	4	US-09-949-016-167924	Sequence 167924, A
C 34	14.8	77.9	601	4	US-09-949-016-189898	Sequence 189898, A
C 35	14.8	77.9	629	4	US-09-513-999C-11622	Sequence 11622, A
C 36	14.8	77.9	1002	4	US-09-252-991A-11872	Sequence 11872, A
C 37	14.8	77.9	1230	4	US-09-252-991A-4767	Sequence 4767, Ap
C 38	14.8	77.9	1356	4	US-09-252-991A-4740	Sequence 4740, Ap
C 39	14.8	77.9	1394	3	US-09-149-476-101	Sequence 101, App
C 40	14.8	77.9	1464	4	US-09-252-991A-11508	Sequence 11508, A
C 41	14.8	77.9	1629	4	US-09-252-991A-11733	Sequence 11733, A
C 42	14.8	77.9	5246	4	US-09-799-451-474	Sequence 474, App
C 43	14.8	77.9	34953	4	US-09-902-540-1263	Sequence 1263, App
C 44	14.8	77.9	35784	4	US-09-949-016-16785	Sequence 16785, A
C 45	14.8	77.9	35784	4	US-09-949-016-16786	Sequence 16786, A
C 46	14.8	77.9	85122	4	US-09-949-016-14693	Sequence 14693, A
C 47	14.8	77.9	119214	4	US-09-949-016-12507	Sequence 12507, A
C 48	14.8	77.9	141560	4	US-09-949-016-16476	Sequence 16476, A
C 49	14.8	77.9	183112	4	US-09-949-016-14184	Sequence 14184, A
C 50	14.8	77.9	227750	4	US-09-949-016-17175	Sequence 17175, A
C 51	14.8	77.9	251769	4	US-09-949-016-13185	Sequence 13185, A
C 52	14.8	77.9	251769	4	US-09-949-016-13186	Sequence 13186, A
C 53	14.8	77.9	266748	4	US-09-949-016-13187	Sequence 13187, A
C 54	14.8	77.9	266748	4	US-09-949-016-13188	Sequence 13188, A
C 55	14.8	77.9	285986	4	US-09-949-016-12287	Sequence 12287, A
C 56	14.8	77.9	288031	4	US-09-949-016-14864	Sequence 14864, A
C 57	14.4	75.8	601	4	US-09-949-016-200201	Sequence 200201, A
C 58	14.4	75.8	605	3	US-08-630-915A-5	Sequence 5, Appl1
C 59	14.4	75.8	605	4	US-09-879-957-5	Sequence 5, Appl1
C 60	14.4	75.8	1053	4	US-09-902-540-2666	Sequence 2666, Ap
C 61	14.4	75.8	1230	4	US-09-902-540-7025	Sequence 7025, Ap
C 62	14.4	75.8	1914	4	US-09-540-236-1278	Sequence 1278, Ap
C 63	14.4	75.8	2226	4	US-09-949-016-4853	Sequence 4853, Ap
C 64	14.4	75.8	2256	4	US-09-540-236-400	Sequence 400, App
C 65	14.4	75.8	2449	4	US-09-710-279-2947	Sequence 2947, Ap
C 66	14.4	75.8	2661	3	US-09-134-001C-1659	Sequence 1659, Ap
C 67	14.4	75.8	2826	4	US-09-695-481-1	Sequence 1, Appl1
C 68	14.4	75.8	2925	4	US-09-695-481-3	Sequence 3, Appl1
C 69	14.4	75.8	3049	4	US-09-710-279-4151	Sequence 4151, Ap
C 70	14.4	75.8	3063	4	US-09-799-451-511	Sequence 511, App
C 71	14.4	75.8	3282	1	US-08-072-574-11	Sequence 11, Appl
C 72	14.4	75.8	3282	1	US-08-486-270-11	Sequence 11, Appl
C 73	14.4	75.8	3282	3	US-08-367-264-11	Sequence 11, Appl
C 74	14.4	75.8	3282	3	US-09-153-757-11	Sequence 11, Appl
C 75	14.4	75.8	3282	4	US-09-459-715-11	Sequence 11, Appl
C 76	14.4	75.8	3371	4	US-09-710-279-3490	Sequence 3490, Ap
C 77	14.4	75.8	4078	4	US-09-016-434-1133	Sequence 1133, Ap
C 78	14.4	75.8	4085	1	US-08-072-574-7	Sequence 7, Appl1
C 79	14.4	75.8	4085	1	US-08-486-270-7	Sequence 7, Appl1
C 80	14.4	75.8	4085	3	US-08-367-264-7	Sequence 7, Appl1
C 81	14.4	75.8	4085	3	US-09-153-757-7	Sequence 7, Appl1
C 82	14.4	75.8	4085	4	US-09-459-715-7	Sequence 7, Appl1
C 83	14.4	75.8	4181	1	US-08-072-574-9	Sequence 9, Appl1
C 84	14.4	75.8	4181	1	US-08-486-270-9	Sequence 9, Appl1
C 85	14.4	75.8	4181	3	US-08-367-264-9	Sequence 9, Appl1
C 86	14.4	75.8	4181	3	US-09-153-757-9	Sequence 9, Appl1
C 87	14.4	75.8	4181	4	US-09-459-715-9	Sequence 9, Appl1
C 88	14.4	75.8	4207	3	US-08-660-148-1	Sequence 1, Appl1
C 89	14.4	75.8	4207	3	US-08-660-148-3	Sequence 3, Appl1
C 90	14.4	75.8	4303	3	US-08-660-148-5	Sequence 5, Appl1
C 91	14.4	75.8	4303	3	US-08-660-148-6	Sequence 6, Appl1
C 92	14.4	75.8	4627	4	US-09-949-016-5553	Sequence 5553, Ap
C 93	14.4	75.8	4919	4	US-09-949-016-999	Sequence 999, App
C 94	14.4	75.8	5588	4	US-09-902-540-621	Sequence 621, App
C 95	14.4	75.8	12061	4	US-09-949-016-16134	Sequence 16134, A
C 96	14.4	75.8	13205	4	US-09-835-811-3	Sequence 3, Appl1
C 97	14.4	75.8	13706	4	US-09-902-540-1124	Sequence 1124, Ap
C 98	14.4	75.8	20608	4	US-09-949-016-16595	Sequence 16595, A
C 99	14.4	75.8	50453	4	US-09-949-016-16642	Sequence 16642, A
C 100	14.4	75.8	51242	4	US-09-949-016-12486	Sequence 12486, A

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OM nucleic - nucleic search, using sw model

Run on: July 5, 2005, 09:16:41 ; Search time 2509.95 Seconds
(without alignments)
288.142 Million cell updates/sec

Title: US-09-943-115A-10

Perfect score: 19

Sequence: 1 ccatcccttcgaatc 19

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gse1:*

9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17.4	91.6	407	8	AZ425215 1M0205N08
2	17.4	91.6	522	8	AZ208099 SP_0136 B
3	17.4	91.6	675	7	CO196969 GEO1_3 A1
4	17.4	91.6	720	9	CR080967 Reverses
5	17.4	91.6	731	7	CF677590 CCAPF13TR
6	17.4	91.6	746	7	CO196968 GEO1_3 A0
7	17.4	91.6	776	7	CO158541 FLN1_7 C0
8	17.4	91.6	897	7	CF690372 CCADBE67R
9	17.4	91.6	909	7	CN783648 EST782339
10	17	89.5	297	2	BB242153 BB242153
11	17	89.5	553	2	AW223646 EST300457
12	17	89.5	573	2	AW223655 EST300466
13	17	89.5	796	7	CV497664 61883.1 M
14	16.4	86.3	180	4	BG954268 CM4-CT066
15	16.4	86.3	370	9	CL249146 ZMWB059
16	16.4	86.3	427	8	BH872947 BB856031
17	16.4	86.3	443	2	BB856031 BB856031
18	16.4	86.3	533	7	CN284843 C284843
19	16.4	86.3	552	5	BH816135 N061A11 P
20	16.4	86.3	555	7	CO682917 DG11-161b
21	16.4	86.3	566	7	CO680769 DG11-120h
22	16.4	86.3	603	7	CO680831 DG11-121g
23	16.4	86.3	613	7	CO689219 DG11-256g
24	16.4	86.3	642	9	CE256161 tigr-g88-

C	25	16.4	86.3	688	4	BG854956	1024041D
	26	16.4	86.3	717	8	BZ026281	
	27	16.4	86.3	723	9	AG556684	Mus musculus
	28	16.4	86.3	746	8	BH920535	odh72a08.
	29	16.4	86.3	773	5	BM071866	BW071866
	30	16.4	86.3	784	8	BZ078746	11499811.
C	31	16.4	86.3	795	6	CD781339	ES652700
	32	16.4	86.3	830	7	CV107995	AGTENCOURT
C	33	16.4	86.3	860	9	CC810943	CV107995
C	34	16.4	86.3	972	4	BG754964	2MMBBC048
C	35	16.4	86.3	1295	4	BG754964	602711662
C	36	16	84.2	115	5	BG756595	602739712
C	37	16	84.2	239	5	BW529774	BW529774
C	38	16	84.2	242	5	BW575995	BW575995
C	39	16	84.2	280	4	BW588106	BW588106
	40	16	84.2	280	4	BM869941	mgnm008xN
C	41	16	84.2	324	4	BI059515	IL3-UT011
C	42	16	84.2	384	6	BY581665	BY581665
C	43	16	84.2	448	1	AV732368	AV732368
C	44	16	84.2	455	5	BW572070	BW572070
C	45	16	84.2	460	5	BW522638	BW522638
C	46	16	84.2	519	5	BW541048	BW541048
C	47	16	84.2	520	5	BW541242	BW541242
	48	16	84.2	551	6	CA694437	wlmk4_pk0
C	49	16	84.2	588	6	CA621700	CA621700
C	50	16	84.2	593	5	BW575916	wlmln_BA00
C	51	16	84.2	601	5	BW540601	BW575916
C	52	16	84.2	602	9	CL705691	SP_Bb004
C	53	16	84.2	687	9	CG105107	PUPZS03TB
C	54	16	84.2	736	8	BH948518	BH948518
C	55	16	84.2	972	3	AY106097	Zea mays
C	56	15.8	83.2	180	1	AJ460084	Forward
C	57	15.8	83.2	225	2	BE071442	CR235044
C	58	15.8	83.2	239	5	BP111712	BB393418
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C	60	15.8	83.2	250	5	BY483735	BB314254
C	61	15.8	83.2	257	2	AW527776	BB314254
C	62	15.8	83.2	260	2	BB477726	BB314254
C	63	15.8	83.2	264	9	CR235044	BB314254
C	64	15.8	83.2	266	2	BB393418	BB314254
C	65	15.8	83.2	270	8	CB314254	BB314254
C	66	15.8	83.2	274	8	CC421069	BB314254
C	67	15.8	83.2	283	2	BB144243	BB314254
C	68	15.8	83.2	300	2	BB084066	BB314254
C	69	15.8	83.2	310	2	BE767140	BB314254
C	70	15.8	83.2	313	2	AW674879	BB314254
C	71	15.8	83.2	316	1	AJ780804	BB314254
C	72	15.8	83.2	328	7	CN350134	BB314254
C	73	15.8	83.2	349	4	BI748761	BB314254
C	74	15.8	83.2	360	1	AJ474044	BB314254
C	75	15.8	83.2	380	6	BZ849771	BB314254
C	76	15.8	83.2	382	6	CB808999	BB314254
C	77	15.8	83.2	384	9	CE450045	BB314254
C	78	15.8	83.2	393	4	BI055427	BB314254
C	79	15.8	83.2	397	9	CG461521	BB314254
C	80	15.8	83.2	403	8	AQ738202	BB314254
C	81	15.8	83.2	403	8	AQ980753	BB314254
C	82	15.8	83.2	404	2	BE359748	BB314254
C	83	15.8	83.2	410	2	BE516065	BB314254
C	84	15.8	83.2	413	6	CD473600	BB314254
C	85	15.8	83.2	416	5	BUG37722	BB314254
C	86	15.8	83.2	419	4	BJ296857	BB314254
C	87	15.8	83.2	419	5	BI100424	BB314254
C	88	15.8	83.2	423	4	BJ290326	BB314254
C	89	15.8	83.2	431	1	AA209317	BB314254
C	90	15.8	83.2	446	7	W78050	BB314254
C	91	15.8	83.2	448	8	AQ598986	BB314254
C	92	15.8	83.2	450	4	BI801394	BB314254
C	93	15.8	83.2	452	4	BJ262247	BB314254
C	94	15.8	83.2	454	8	BZ925155	BB314254
C	95	15.8	83.2	457	4	BM452823	BB314254
C	96	15.8	83.2	460	8	AQ696472	BB314254
C	97	15.8	83.2	461	2	BE775987	BB314254
C	98	15.8	83.2	464	5	BX485827	BB314254

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OM nucleic - nucleic search, using sw model

Run on: July 5, 2005, 09:16:41 ; Search time 329.333 Seconds
(without alignments)
341.524 Million cell updates/sec

Title: US-09-943-115A-10
Perfect score: 19
Sequence: 1 ccattcccttcgaatc 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : N_Geneseq_16Dec04:*
1: Geneseqn1980a:*
2: Geneseqn1990a:*
3: Geneseqn2000a:*
4: Geneseqn2001a:*
5: Geneseqn2001b:*
6: Geneseqn2002a:*
7: Geneseqn2002b:*
8: Geneseqn2003a:*
9: Geneseqn2003b:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004a:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	6	ABK68754 PCR prime
2	19	100.0	1345	2	AAX28296 Human CYP
3	19	100.0	1345	2	AAX257019 Nucleic a
4	19	100.0	1345	3	AAX257020 Nucleic a
5	19	100.0	1345	6	ABK68745 5'-flanki
6	19	100.0	1345	12	ADJ84441 Human phe
7	19	100.0	6101	13	ADS89077 Human CYP
8	19	100.0	12983	6	AD41239 Human CYP
9	19	100.0	13035	8	AD51997 Human CYP
10	19	100.0	15185	8	AD52000 Human CYP
11	19	100.0	39071	12	ADM97420 Prostata
12	19	100.0	96960	8	ACF62734 Cancer ba
13	19	100.0	96960	8	ADB20849 MRPL-base
14	19	100.0	96960	10	ADB87938 Human UGT
15	19	100.0	96960	10	ADB96921 Human MDR
16	19	100.0	96960	10	ADB92112 Human MDR
17	19	100.0	123785	10	ABX77171 DNA seque
18	17.4	91.6	6101	13	ADS89689 Oligonuc
19	17.4	91.6	6101	13	ADS89415 Oligonuc
20	16.4	86.3	309	4	AAH37148 Human col

21	16.4	86.3	520	12	ACH75108
22	16.4	86.3	1012	6	AAD36215
23	16.4	86.3	7966	4	ABL19154
24	16.4	86.3	8943	6	ABK39966
25	16.4	86.3	9903	4	ABL09916
26	16.4	86.3	11186	6	AAD41242
27	16.4	86.3	11186	6	AAD36213
28	16.4	86.3	256493	11	ACN44514
29	16	84.2	812	2	AAX16385
30	15.8	83.2	389	3	AAC17802
31	15.8	83.2	446	6	ABL68081
32	15.8	83.2	446	6	ABL65126
33	15.8	83.2	446	6	ABL66878
34	15.8	83.2	446	6	ABT11074
35	15.8	83.2	501	6	AAS61631
36	15.8	83.2	542	4	AAS44754
37	15.8	83.2	567	12	ADQ81633
38	15.8	83.2	567	12	ADQ81635
39	15.8	83.2	594	10	ADH84190
40	15.8	83.2	752	5	ABV12884
41	15.8	83.2	1717	4	AAS44582
42	15.8	83.2	1990	10	ADA52447
43	15.8	83.2	2214	10	ADA53564
44	15.8	83.2	2470	4	AAH16228
45	15.8	83.2	2686	5	AAS73640
46	15.8	83.2	3134	12	ADQ87636
47	15.8	83.2	5840	2	AAX12968
48	15.8	83.2	5840	6	ABS98763
49	15.8	83.2	185555	11	ACN45180
50	15.4	81.1	253	12	ADF99569
51	15.4	81.1	323	8	ABS57436
52	15.4	81.1	330	8	ABS56354
53	15.4	81.1	2139	8	ACA43015
54	15.4	81.1	2380	12	ADI19357
55	15.4	81.1	2380	12	ADJ65942
56	15.4	81.1	3018	8	ADA70619
57	15.4	81.1	4821	4	AAH62756
58	15.4	81.1	5872	4	ABL06090
59	15.4	81.1	45839	6	AAD42191
60	15.4	81.1	77425	6	ABK83502
61	15.4	81.1	110000	10	ADG70184
62	15.4	81.1	175338	11	ACN45088
63	15.4	81.1	188794	12	ADQ59476
64	15.4	81.1	305107	4	AAH62689
65	15.4	81.1	349981	10	ADC87619
66	15	78.9	447	3	AAA60920
67	15	78.9	882	11	ACH96896
68	15	78.9	1230	3	AAH13712
69	15	78.9	1389	3	AAZ91264
70	15	78.9	2380	3	AAV07911
71	15	78.9	2381	2	AAV07911
72	15	78.9	2494	3	AAZ91253
73	14.8	77.9	31	4	AAI30350
74	14.8	77.9	139	12	ACH86962
75	14.8	77.9	259	12	ADQ55883
76	14.8	77.9	321	6	ABK73598
77	14.8	77.9	402	9	AAI84778
78	14.8	77.9	402	9	ACH49084
79	14.8	77.9	461	9	ACH27948
80	14.8	77.9	482	9	ACH27904
81	14.8	77.9	513	6	ABK70158
82	14.8	77.9	548	7	ADS31235
83	14.8	77.9	578	6	ABL36882
84	14.8	77.9	581	12	ACH73231
85	14.8	77.9	583	13	ADH64038
86	14.8	77.9	601	12	ADL15860
87	14.8	77.9	616	8	ACA45195
88	14.8	77.9	616	12	ADQ09663
89	14.8	77.9	629	3	AAC07547
90	14.8	77.9	638	8	ABZ53978
91	14.8	77.9	862	6	ABQ46057
92	14.8	77.9	862	6	ABQ46056
93	14.8	77.9	869	12	ADJ40322

ACH75108 Human gen
Aad36215 Human pro
Abi19154 Drosophil
Abk39966 Humar che
Abk09916 Drosophil
Aad41242 Human CYP
Aad36213 Human CYP
Aad44514 Human gen
Aad16385 Human gen
Aad17802 Human sec
Abi68081 Ovary can
Abi65126 Lung can
Abi66878 Lung can
Abi11074 Human bre
Aas61631 Lung smal
Aas44754 Human con
Aad81633 Enterococ
Aad81635 Enterococ
Adh84190 Enterococ
Abv12884 Human pro
Aas44582 Human ful
Ada52447 Human cod
Ada53564 Human cod
Aah16228 Human CDN
Aas73640 DNA enco
Adq87636 Human tum
Aax12968 Enterococ
Abs98763 Enterococ
Acn45180 Mouse gen
Adf99569 Nicotiana
Abf99569 Metalloth
Abz56354 Aspergill
Aca43015 Prokaryot
Adi19357 Soybean t
Adj65942 soybean t
Ada70619 Rice gene
Aah62756 Shrimp wh
Abi06090 Drosophil
Aad42191 Human rgy
Abk83502 Human CDN
Adg70184 DNA of BA
Acn45088 Mouse gen
Adq59476 Human can
Aah62689 Shrimp wh
Adc87619 Human GPC
Aaa60920 Phaneroch
Ach96896 Klebsiell
Aaa13712 Human pro
Aaz91264 Fumarate
Aav07911 Mouse cys
Aaz91253 Bacterium
Aai30350 Human ein
Ach86962 Human gen
Adq05583 Soybean t
Abk73598 Bacillus
Aai84778 Human pol
Ach49084 Human leu
Ach27948 Human adu
Ach27904 Human adu
Abk70158 Human lun
Ads31235 Human gen
Abi36882 Human col
Ach73231 Human gen
Adh64038 Cotton cd
Adl15860 Novel tra
Aca45195 Prokaryot
Adq09663 Rice 13kd
Aac07547 Human sec
Abz53978 Aspergill
Abq46057 Oligonuc
Abq46056 Oligonuc
Adj40322 Plant cDN